



SEQUENCE LISTING

<110> EPIGENOMICS AG

<120> Method for relative quantification of methylation
of cytosin bases in DNA samples

<130> 81796

<140> US10/057,776

<141> 2002-01-25

<150> PCT/DE00/02490

<151> 2000-07-25

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1

aactcccaa tactacaacc

20

<210> 2

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2

aaaatacaca aacrtccca

20

<210> 3

<211> 28

<212> DNA

<213> Homo sapiens

<400> 3

ctacaataat ctttcttcaa cataactta

28

<210> 4

<211> 28

<212> DNA

<213> Homo sapiens

<400> 4

taaaaactat cccataataa ctcccaac

28

<210> 5
<211> 28
<212> DNA
<213> Homo sapiens

<400> 5
caagcatgct gaagaaagac cactgcag 28

<210> 6
<211> 28
<212> DNA
<213> Homo sapiens

<400> 6
tggaactgt ccataataa ctccaac 28

<210> 7
<211> 20
<212> DNA
<213> Homo sapiens

<400> 7
ggctgcagca ctggggagcc 20

<210> 8
<211> 20
<212> DNA
<213> Homo sapiens

<400> 8
ggctccccag tgctgcagcc 20

<210> 9
<211> 28
<212> DNA
<213> Homo sapiens

<400> 9
taagtatgtt gaagaaagat tattgtag 28

<210> 10
<211> 19
<212> DNA
<213> Homo sapiens

<400> 10
aactcccaa tactacaac 19

<210> 11
<211> 20
<212> DNA

<213> Homo sapiens

<400> 11

tgggagyggtt tgtgtatttt

20